

09/973, 994
4/04/05

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 02:47:25 ; Search time 971.806 Seconds
(without alignments)
9193.767 Million cell

updates/sec

Title: US-09-973-994-79
Perfect score: 307
Sequence: 1 ggtgcgatcctagaattgca.....gccatcactcggatcgcacc 307

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*

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30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query					Description
No.	Score	Match	Length	DB	ID		

sapi	1	22	7.2	131427	2	AF121897	AF121897 Homo
sapi	2	22	7.2	185982	2	AC073231	AC073231 Homo
sapi	3	22	7.2	340000	9	HS21C080	AL163280 Homo
sapi	4	21	6.8	185775	2	AL772276	AL772276 Mus
muscu	5	20	6.5	65711	2	AC117583	AC117583 Mus
muscu	6	20	6.5	87971	2	AC117094	AC117094
Rattus no	7	20	6.5	94820	2	AC119140	AC119140
Rattus no	8	20	6.5	140466	2	AC095152	AC095152
Rattus no	9	20	6.5	141017	2	AC116962	AC116962
Dictyoste	10	20	6.5	151374	2	AC111772	AC111772
Rattus no	11	20	6.5	274947	2	AL731766	AL731766 Mus
muscu	12	19	6.2	1627	8	ZMKN1	X61308 Z.mays
Knot	13	19	6.2	5200	1	AY005468	AY005468
Pseudoalt	14	19	6.2	33184	3	U70856	U70856
Caenorhabdi	15	19	6.2	70162	2	AC026568	AC026568 Homo
sapi	16	19	6.2	85458	2	AC106054	AC106054
Rattus no	17	19	6.2	89207	2	AC124098	AC124098 Mus
muscu	18	19	6.2	104600	9	AP001166	AP001166 Homo

sapi						
c 19	19	6.2	108400	9	AC005193	AC005193 Homo
sapi						
c 20	19	6.2	110000	2	AC129176_2	Continuation
(3 of						
21	19	6.2	123277	9	AC005016	AC005016 Homo
sapi						
22	19	6.2	134778	9	AC078848	AC078848 Homo
sapi						
c 23	19	6.2	134979	9	AL359963	AL359963
Human DNA						
24	19	6.2	135607	2	AC115922	AC115922 Mus
muscu						
c 25	19	6.2	136283	9	AP005202	AP005202 Homo
sapi						
c 26	19	6.2	136791	9	AC079896	AC079896 Homo
sapi						
c 27	19	6.2	140702	2	AC068420	AC068420 Homo
sapi						
28	19	6.2	141866	9	AL451062	AL451062
Human DNA						
29	19	6.2	143595	2	AC027563	AC027563 Homo
sapi						
30	19	6.2	148083	9	AF111170	AF111170 Homo
sapi						
c 31	19	6.2	152320	9	AC084377	AC084377 Homo
sapi						
32	19	6.2	155711	3	VYIVD10	AL360354
Plasmodiu						
c 33	19	6.2	156471	2	AC013568	AC013568 Homo
sapi						
34	19	6.2	162743	4	AC091728	AC091728 Bos
tauru						
c 35	19	6.2	162810	9	AC006382	AC006382 Homo
sapi						
36	19	6.2	162900	2	AC123889	AC123889
Rattus no						
37	19	6.2	164528	2	AC016800	AC016800 Homo
sapi						
38	19	6.2	171325	9	AC079345	AC079345 Homo
sapi						
c 39	19	6.2	173292	9	AL139085	AL139085
Human DNA						
c 40	19	6.2	173394	9	AC025040	AC025040 Homo
sapi						
41	19	6.2	176469	2	AC121034	AC121034
Rattus no						
c 42	19	6.2	182035	2	AC068040	AC068040 Homo
sapi						
c 43	19	6.2	183328	2	AC101773	AC101773 Mus
muscu						
44	19	6.2	193516	2	AC117207	AC117207 Mus
muscu						
c 45	19	6.2	194769	2	AC113489	AC113489 Mus
muscu						

LOCUS PIAEMB2R 861 bp mRNA linear PLN 16-JUN-1999

DEFINITION *Picea glauca* late embryogenesis abundant protein (EMB2) mRNA, complete cds.

ACCESSION L47115

VERSION L47115.1 GI:1350521

KEYWORDS late embryogenesis abundant protein.

SOURCE *Picea glauca* (white spruce)

ORGANISM *Picea glauca*
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; *Picea*.

REFERENCE 1 (bases 1 to 861)

AUTHORS Dong, J.Z. and Dunstan, D.I.

TITLE Cloning and characterization of six embryogenesis-associated cDNAs from somatic embryos of *Picea glauca* and their comparative expression during zygotic embryogenesis

JOURNAL Plant Mol. Biol. 39 (4), 859-864 (1999)

PUBMED 10350098

REFERENCE 2 (bases 1 to 861)

AUTHORS Dong, J.Z. and Dunstan, D.I.

TITLE Direct Submission

JOURNAL Submitted (30-MAY-1996) Crop Science, Horticulture Research International, East Malling, West Malling, Kent ME19 6BJ, UK

FEATURES

	Location/Qualifiers
source	1..861 /organism="Picea glauca" /mol_type="mRNA" /db_xref="taxon:3330" /note="(vector lambda zap)"
gene	1..861 /gene="EMB2"
5'UTR	<1..54 /gene="EMB2"
CDS	55..648 /gene="EMB2" /codon_start=1 /product="late embryogenesis abundant protein" /protein_id="AAB01563.1" /db_xref="GI:1350522" /translation="MAIARLLREICTKPTRFKRESSHPTLNLRFS S S LKNPIKSTLNS SSEQQEALTSNGSSKHLFNATLKFSGRICTWGAEIGNLGSPFEIDRRYFSVDSSNLDY SKEVDEINAKFAEAREELEMMESKETVYFDEEAETARDAVKQTLEMF DALLTKLPEA ERGAVQ RSMGLKMEQLKAELS QVKRSKILCTP WMYFY"
3'UTR	649..861 /gene="EMB2"
polyA_site	861 /gene="EMB2"

ORIGIN

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1 gctttgagag accacggttt cagggtttta acaggagcag ggtttcacgc cgcgatggcg
61 attgcgcggc ttttgcgaga gatctgcaca aaaccaccca ggtttaagcg agagtcctct
121 catccaaccc ttaacctccg attctcaagc ccgctgaaaa accccatcaa gtcaacccta
181 aattcgtctt ctgaacagca agaagccctt acttcaaacg gatcctcaaa acatctcttc
241 aacgcaactc tcaaattcag cggacggatt tgtacttggg gcgcggaaat aggtaatattg
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421 gcaatggagt ctaaggaaac gttttatttt gacgaggaag ccgagactgc cagagacgct
481 gtgaaacaaa ccctagaaat gttc gatgcc cttttgacta aattgccga agccgaaaga
541 ggtgctgtac agaggtccat gggattgaag atggaacagc ttaaagcaga gctttcacia
601 gttaaacgga gtaaaattct ttgcaccccc tggatgtatt tttattagtt ttggcatttt
661 ggggggttta gtttggcatt caagggccta taattattga ttctgtatga attgagtgat
721 tcgagttatt gcgtagggcg atttcacaat gcattcagct gatataaatt tttggcgctg

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781 gaatttttcg ttatagaaac aattaatgct gtaaggcat tcttcttttg tgcttcatgt
841 taagcttatc ataatttctt t

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LOCUS PIAEMB6R 942 bp DNA linear PLN 16-JUN-1999

DEFINITION Picea glauca late embryogenesis abundant protein (EMB6) mRNA, complete cds.

ACCESSION L47116

VERSION L47116.1 GI:1350540

KEYWORDS late embryogenesis abundant protein.

SOURCE Picea glauca (white spruce)

ORGANISM Picea glauca
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.

REFERENCE 1 (bases 1 to 942)

AUTHORS Dong, J.Z. and Dunstan, D.I.

TITLE Cloning and characterization of six embryogenesis-associated cDNAs from somatic embryos of Picea glauca and their comparative expression during zygotic embryogenesis

JOURNAL Plant Mol. Biol. 39 (4), 859-864 (1999)

PUBMED 10350098

REFERENCE 2 (bases 1 to 942)

AUTHORS Dong, J.Z. and Dunstan, D.I.

TITLE Direct Submission

JOURNAL Submitted (30-MAY-1996) Crop Science, Horticulture Research International, East Malling, West Malling, Kent ME19 6BJ, UK

FEATURES

	Location/Qualifiers
source	1..942 /organism="Picea glauca" /mol_type="genomic DNA" /db_xref="taxon:3330" /dev_stage="mature somatic embryo"
gene	1..942 /gene="EMB6"
mRNA	<1..942 /gene="EMB6"
5'UTR	<1..49 /gene="EMB6"
CDS	50..769 /gene="EMB6" /codon_start=1 /product="late embryogenesis abundant protein" /protein_id="AAB01569.1" /db_xref="GI:1350541" /translation="MKEAGECFTLGRTIGRKRNAMSAENWQKEERAVDDSRVKFSFS DDRSGPGRILRHRPDEEEVCVTPVKPCPILAAGKDENSAGRDLASLALDVLVEVCNL GHHELEPLTRVSKDFKQAVKVANETHFGFKTPDPVRRPNRSLFLNQSHANSASGSDSP SRWPATPKAPKR VVKHRNLLASDKEFADLSRVLF LDGNQPSGVDVDAEHTICLKPGI ATNRALFSTDELSGALSRHCI"
3'UTR	770..942 /gene="EMB6"
polyA_site	942 /gene="EMB6"

ORIGIN

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61 aggggagtggt ttcacactcg gtcgcactat tggcagaaaag aggaatgcga tgtcggctgc
121 ggagaattgg cagaaagagg aacgcgctgt cgacgacagt agggttaaat ttagcttttc
181 ggatgatcgt tcaggacctg ggagaatcct acgccacagg cctgacgagg aggaagtttg
241 cgtcactccg gtgaagccct gccctatact tgctgctggt aaagatgaga attcggcccg
301 aagggacttg gcgtcttttg ctttagatgt cttggtagag gtagtctgta acctcgggca
361 ccatgaactc gagccgttaa ctgcgctttc aaaggatttc aaacaagcgg ttaaagttgc
421 taatgaaacg cattttggtt ttaaaacccc ggatcctgtg cggagaccta atcgttcgct
481 attttttaaat caaagccatg caaattccgc ttccggaagt gatagtccat ctcgatggcc
541 tgcaacgccg aaggcaccga aacgtgtagt gaagcatcgg aatcttctcg cgagtgataa

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601 agaattcgca gatttaagca gagtgctctt tctggatggc aatcagccat ccggcggtga
661 tgttgttgat gcagagcata ctatttgctt gaagccgggc attgctacaa acagggcttt
721 atttagcacg gatgagcttt ctggggcatt gtcccgtcac tgcatataga aagtttacga
781 agggaatgcg ggatcctccc attttttttt tcaagtgttg ggaaaacagg cggaggagga
841 ttttatgggg agaattctcac ttctcgtgag ctttccaac cagttttatt ttttttaggt
901 taaactctgt aaaaacaaat cttcaaccag ttttggggtc cc

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